SEQUENCE LISTING

<110> The Government of the United States

<120> Bovine Adeno-Associated Viral (BAAV)
      Vector and Uses Thereof

<130> 14014.0417P1

<140> Unassigned
<141> 2004-12-06

<150> 60/526,786
<151> 2003-12-04

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 4694
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 1
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tcaaagagct gccagacgac ggccctctgg gccgtcgccc ccccaatcga gccagcgaac   120
gagcgaacgc gacaggggggg ggagtgccac actctctagc aagggggttt tgtaggtggt   180
gatgtcattg ttgatgtcat tatagttgtc acgcgatagt taatgattaa cagtcatgtg   240
atgtgtgtta tccaatagga tgaaagcgcg cgaatgagat ctcgcgagac ttccggggta   300
taaaaggggt gagtgaacga gcccgccgcc attctctgct ctggactgct agaggaccct   360
cgctgccatg gctaccttct atgaagtcat tgttcgcgtt ccatttgatg tggaagagca   420
cctgcctgga atttctgaca actttgtaga ctgggtaact ggtcaaattt gggagctgcc   480
tcccgagtca gatttgaatt tgactctgat tgagcagcct cagctgacgg tggctgacag   540
aattcgccgc gtgttcctgt acgagtggaa caaatttttcc aagcaggaga gcaaattctt   600
tgtgcagttt gaaaagggat ctgaatattt tcatctgcac acgctcgtgg agacctccgg   660
catctcttct atggtccttg gccgctacgt gagtcagatt cgcgcccagc tggtgaaggt   720
ggtgttccag aacattgagc cgcggattaa cgactgggtc gccatcacca aggtaaagaa   780
gggcggagcc aataaggtgg tggattctgg gtatattccc gcctacctgc tgccgaaggt   840
ccaaccagag cttcagtggg cgtggactaa cctcgaagag tataaattgg ccgccctcaa   900
tctggaggag cgcaaacggc tcgtcgctca gtttcagctt gagtcctcgc agcgctcgca   960
agaggcatct tcccagaggg acgtttcggc tgaccggtc atcaagagca agacttccca   1020
gaaatacatg gcgctggtaa gctggctggt ggaacatggc atcacttccg agaagcagtg   1080
gattcaggag aatcaggaga gctacctgtc ctccaactcc acgggaaact ctcggagcca   1140
gattaaagcc gcgcttgaca acgcgtcaaa aattatgagt ctgaccaaat ctgcctcaga   1200
ctatctcgtg ggacagactg ttccagagga catttctgaa aacagaatct ggcagatttt   1260
tgatctcaac ggctacgacc cggcatacgc gggctctgtt ctctacggct ggtgcactcg   1320
cgcctttgga aagaggaaca ccgtctggct gtatggaccc gcgaccaccg gaaagaccaa   1380
catcgcggaa gccatctctc acaccgtgcc cttttatggc tgtgtgaact ggactaatga   1440
gaactttccc tttaatgact gtgtggaaaa aatgttgatc tggtgggagg agggaaagat   1500
gaccagcaag gtggtggaac cgccaaggc catcttgggg gggtctagag tacgagtgga   1560
tcaaaaatgt aaatcctctg tacaagtaga ctctaccccg gtgattatca cctccaatac   1620
taacatgtgt gtggtggtgg atgggaactc cacgaccttt gaacaccagc agccgctgga   1680
agaccgcatg ttcagatttg aactcatgcg cggctcccg ccagattttg caagattac   1740
caagcaggaa gtcaaagact tttttgcttg gcaaaggtc aaccaggtgc cggtgactca   1800
cgagtttatg gttcccaaga aagtggcggg aactgagagg gcggagactt ctagaaaacg   1860
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```
cccactggat gacgtcacca ataccaacta taaaagtccg gagaagcggg cccggctctc      1920
agttgttcct gagacgcctc gcagttcaga cgtgcctgta gagcccgctc ctctgcgacc      1980
tctcaactgg tcttccaggt atgaatgcag atgtgactat catgctaaat ttgactctgt      2040
aacggggaa tgtgacgagt gtgaatattt gaatcggggc aaaaatggct gtatctttca      2100
taatgctaca cattgtcaaa tttgtcacgc tgttcctcca tgggaaaagg aaaatgtgtc      2160
agattttaat gattttgatg actgtaataa agagcagtaa ataaagtgag tagtcatgtc      2220
ttttgttgac caccctccag attggttgga atcgatcggc gacggctttc gtgaatttct      2280
cggccttgag gcgggtcccc cgaaacccaa ggccaatcaa cagaagcaag ataacgctcg      2340
aggtcttgtg cttcctgggt acaagtatct tggtcctggg aacggccttg ataagggcga      2400
tcctgtcaat tttgctgacg aggttgcccg agagcacgac ctctcctacc agaaacagct      2460
tgaggcgggc gataacccctt acctcaagta caaccacgcg gacgcagagt ttcaggagaa      2520
actcgcttct gacacttctt ttgggggaaa ccttgggaag gctgtttttcc aggctaaaaa      2580
gaggattctc gaacctcttg gcctggttga gacgccggat aaaacggcgc ctgcggcaaa      2640
aaagaggcct ctagagcaga gtcctcaaga gccagactcc tcgagcggag ttggcaagaa      2700
aggcaaacag cctgccagaa agagactcaa ctttgacgac gaacctggag ccggagacgg      2760
gcctccccca gaaggaccat cttccggagc tatgtctact gagactgaaa tgcgtgcagc      2820
agctggcgga aatggtggcg atgcgggaca aggtgccgag ggagtgggta atgcctccgg      2880
tgattggcat tgcgattcca cttggtcaga gagccacgtc accaccacct caacccgcac      2940
ctgggtcctg ccgacctaca acaaccacct gtacctgcgg ctcggctcga gcaacgccag      3000
cgacacct tc aacggattct ccacccctg gggatacttt gactttaacc gcttccactg      3060
ccacttctcg ccaagagact ggcaaaggct catcaacaac cactggggac tgcgccccaa      3120
aagcatgcaa gtccgcatct tcaacatcca agttaaggag gtcacgacgt ctaacgggga      3180
gacgaccgta tccaacaacc tcaccagcac ggtccagatc tttgcggaca gcacgtacga      3240
gctcccgtac gtgatggatg caggtcagga gggcagcttg cctccttttcc ccaacgacgt      3300
gttcatggtg cctcagtacg ggtactgcgg actggtaacc ggaggcagct ctcaaaacca      3360
gacagacaga aatgccttct actgtctgga gtactttccc agccagatgc tgagaaccgg      3420
aaacaacttt gagatggtgt acaagtttga aaacgtgccc ttccactcca tgtacgctca      3480
cagccagagc ctggataggc tgatgaaccc gctgctggac cagtacctgt gggagctcca      3540
gtctaccacc tctggaggaa ctctcaacca gggcaattca gccaccaact ttgccaagct      3600
gaccaaaaca aactttttctg ctaccgcaa aaaactggctc ccggggccca tgatgaagca      3660
gcagagattc tccaagactg ccagtcaaaa ctacaagatt ccccagggaa gaaacaacag      3720
tctgctccat tatgagacca gaactaccct cgacggaaga tggagcaatt ttgccccggg      3780
aacggccatg gcaaccgcag ccaacgacgc caccgacttc tctcaggccc agctcatctt      3840
tgcggggccc aacatcaccg gcaacaccac cacagatgcc aataacctga tgttcacttc      3900
agaagatgaa cttagggcca ccaaccccg ggacactgac ctgtttggcc acctggcaac      3960
caaccagcaa aacgccacca ccgttcctac cgtagacgac gtggacggag tcggcgtgta      4020
cccgggaatg gtgtggcagg acagagacat ttactaccaa gggcccattt gggccaaaat      4080
tccacacacg gatggacact ttcacccgtc tcctctcatt ggcggatttg gactgaaaag      4140
cccgcctcca caaatattca tcaaaaacac tcctgtaccc gccaatcccg caacgacctt      4200
ctctccggcc agaatcaaca gcttcatcac ccagtacagc accggacagg tggctgtcaa      4260
aatagaatgg gaaatccaga aggagcggtc caagagatgg aacccagagg tccagttcac      4320
gtccaactac ggagcacagg actcgcttct ctgggctccc gacaacgccg gagcctacaa      4380
agagcccagg gccattggat cccgatacct caccaaccac ctctagccca attctgttgc      4440
ataccctcaa taaaccgtgt attcgtttca gtaaaatact gcctcttgtg tcattcggc      4500
gtacaacagc ttacaacaac aacaaaaccc ccttgctaga gagtgtggca ctcccccccc      4560
tgtcgcgttc gctcgttcgc tggctcgatt ggggggtgg cagctcaaag agctgccaga      4620
cgacggccct ctgggccgtc gccccccaa tcgagccagc gaacgagcga acgcgacagg      4680
ggggggagtg ccac                                                       4694
```

<210> 2
<211> 1833
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 2
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atggctacct tctatgaagt cattgttcgc gttccatttg atgtggaaga gcacctgcct       60
ggaatttctg acaactttgt agactgggta actggtcaaa tttgggagct gcctcccgag      120
```

```
tcagatttga atttgactct gattgagcag cctcagctga cggtggctga cagaattcgc    180
cgcgtgttcc tgtacgagtg gaacaaattt tccaagcagg agagcaaatt ctttgtgcag    240
tttgaaaagg gatctgaata ttttcatctg cacacgctcg tggagacctc cggcatctct    300
tctatggtcc ttggccgcta cgtgagtcag attcgcgccc agctggtgaa ggtggtgttc    360
cagaacattg agccgcggat taacgactgg gtcgccatca ccaaggtaaa gaagggcgga    420
gccaataagg tggtggattc tgggtatatt cccgcctacc tgctgccgaa ggtccaacca    480
gagcttcagt gggcgtggac taacctcgaa gagtataaat tggccgccct caatctggag    540
gagcgcaaac ggctcgtcgc tcagtttcag cttgagtcct cgcagcgctc gcaagaggca    600
tcttcccaga gggacgtttc ggctgacccg gtcatcaaga gcaagacttc ccagaaatac    660
atggcgctgg taagctggct ggtggaacat ggcatcactt ccgagaagca gtggattcag    720
gagaatcagg agagctacct gtccttcaac tccacgggaa actctcggag ccagattaaa    780
gccgcgcttg acaacgcgtc aaaaattatg agtctgacca aatctgcctc agactatctc    840
gtgggacaga ctgttccaga ggacatttct gaaaacagaa tctggcagat ttttgatctc    900
aacggctacg acccggcata cgcgggctct gttctctacg gctggtgcac tcgcgccttt    960
ggaaagagga acaccgtctg gctgtatgga cccgcgacca ccggaaagac caacatcgcg   1020
gaagccatct ctcacaccgt gccctttttat ggctgtgtga ctggactaa tgagaacttt   1080
cccttttaatg actgtgtgga aaaaatgttg atctggtggg aggagggaaa gatgaccagc   1140
aaggtggtgg aacccgccaa ggccatcttg ggggggtcta gagtacgagt ggatcaaaaa   1200
tgtaaatcct ctgtacaagt agactctacc ccggtgatta tcacctccaa tactaacatg   1260
tgtgtggtgg tggatgggaa ctccacgacc tttgaacacc agcagccgct ggaagaccgc   1320
atgttcagat ttgaactcat gcggcggctc ccgccagatt ttggcaagat taccaagcag   1380
gaagtcaaag actttttttgc ttgggcaaag gtcaaccagg tgccggtgac tcacgagttt   1440
atggttccca agaaagtggc gggaactgag agggcggaga cttctagaaa acgcccactg   1500
gatgacgtca ccaataccaa ctataaaagt ccggagaagc gggcccggct ctcagttgtt   1560
cctgagacgc ctcgcagttc agacgtgcct gtagagcccg ctcctctgcg acctctcaac   1620
tggtcttcca ggtatgaatg cagatgtgac tatcatgcta aatttgactc tgtaacgggg   1680
gaatgtgacg agtgtgaata tttgaatcgg ggcaaaaatg ctgtatctt tcataatgct   1740
acacattgtc aaatttgtca cgctgttcct ccatgggaaa aggaaaatgt gtcagatttt   1800
aatgattttg atgactgtaa taaagagcag taa                                1833
```

```
<210> 3
<211> 610
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 3
Met Ala Thr Phe Tyr Glu Val Ile Val Arg Val Pro Phe Asp Val Glu
1               5                   10                  15
Glu His Leu Pro Gly Ile Ser Asp Asn Phe Val Asp Trp Val Thr Gly
            20                  25                  30
Gln Ile Trp Glu Leu Pro Pro Glu Ser Asp Leu Asn Leu Thr Leu Ile
        35                  40                  45
Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu
    50                  55                  60
Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln
65                  70                  75                  80
Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr
                85                  90                  95
Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg
            100                 105                 110
Ala Gln Leu Val Lys Val Val Phe Gln Asn Ile Glu Pro Arg Ile Asn
        115                 120                 125
Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val
    130                 135                 140
Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro
145                 150                 155                 160
```

```
Glu Leu Gln Trp Ala Trp Thr Asn Leu Glu Glu Tyr Lys Leu Ala Ala
            165             170                 175
Leu Asn Leu Glu Glu Arg Lys Arg Leu Val Ala Gln Phe Gln Leu Glu
            180             185                 190
Ser Ser Gln Arg Ser Gln Glu Ala Ser Ser Gln Arg Asp Val Ser Ala
            195             200             205
Asp Pro Val Ile Lys Ser Lys Thr Ser Gln Lys Tyr Met Ala Leu Val
    210             215             220
Ser Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln
225             230             235                 240
Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr Gly Asn Ser Arg
                245             250             255
Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys Ile Met Ser Leu
            260             265             270
Thr Lys Ser Ala Ser Asp Tyr Leu Val Gly Gln Thr Val Pro Glu Asp
            275             280             285
Ile Ser Glu Asn Arg Ile Trp Gln Ile Phe Asp Leu Asn Gly Tyr Asp
    290             295             300
Pro Ala Tyr Ala Gly Ser Val Leu Tyr Gly Trp Cys Thr Arg Ala Phe
305             310             315                 320
Gly Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala Thr Thr Gly Lys
                325             330             335
Thr Asn Ile Ala Glu Ala Ile Ser His Thr Val Pro Phe Tyr Gly Cys
            340             345             350
Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Glu Lys
            355             360             365
Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Ser Lys Val Val Glu
370             375             380
Pro Ala Lys Ala Ile Leu Gly Gly Ser Arg Val Arg Val Asp Gln Lys
385             390             395                 400
Cys Lys Ser Ser Val Gln Val Asp Ser Thr Pro Val Ile Ile Thr Ser
                405             410             415
Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser Thr Thr Phe Glu
            420             425             430
His Gln Gln Pro Leu Glu Asp Arg Met Phe Arg Phe Glu Leu Met Arg
    435         ·       440             445
Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln Glu Val Lys Asp
    450             455             460
Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val Thr His Glu Phe
465             470             475                 480
Met Val Pro Lys Lys Val Ala Gly Thr Glu Arg Ala Glu Thr Ser Arg
                485             490             495
Lys Arg Pro Leu Asp Asp Val Thr Asn Thr Asn Tyr Lys Ser Pro Glu
            500             505             510
Lys Arg Ala Arg Leu Ser Val Val Pro Glu Thr Pro Arg Ser Ser Asp
            515             520   _         525
Val Pro Val Glu Pro Ala Pro Leu Arg Pro Leu Asn Trp Ser Ser Arg
    530             535             540
Tyr Glu Cys Arg Cys Asp Tyr His Ala Lys Phe Asp Ser Val Thr Gly
545             550             555                 560
Glu Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys Asn Gly Cys Ile
 ·          565             570                 575
Phe His Asn Ala Thr His Cys Gln Ile Cys His Ala Val Pro Pro Trp
            580             585                 590
Glu Lys Glu Asn Val Ser Asp Phe Asn Asp Phe Asp Asp Cys Asn Lys
            595             600             605
Glu Gln
    610
```

<210> 4
<211> 1173

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 4
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atggcgctgg taagctggct ggtggaacat ggcatcactt ccgagaagca gtggattcag      60
gagaatcagg agagctacct gtccttcaac tccacgggaa actctcggag ccagattaaa     120
gccgcgcttg acaacgcgtc aaaaattatg agtctgacca aatctgcctc agactatctc     180
gtgggacaga ctgttccaga ggacatttct gaaaacagaa tctggcagat ttttgatctc     240
aacggctacg acccggcata cgcgggctct gttctctacg gctggtgcac tcgcgccttt     300
ggaaagagga acaccgtctg gctgtatgga cccgcgacca ccggaaagac caacatcgcg     360
gaagccatct ctcacaccgt gcccttttat ggctgtgtga actggactaa tgagaacttt     420
ccctttaatg actgtgtgga aaaaatgttg atctggtggg aggagggaaa gatgaccagc     480
aaggtggtgg aacccgccaa ggccatcttg ggggggtcta gagtacgagt ggatcaaaaa     540
tgtaaatcct ctgtacaagt agactctacc ccggtgatta tcacctccaa tactaacatg     600
tgtgtggtgg tggatgggaa ctccacgacc tttgaacacc agcagccgct ggaagaccgc     660
atgttcagat ttgaactcat gcggcggctc ccgccagatt ttggcaagat taccaagcag     720
gaagtcaaag acttttttgc ttgggcaaag gtcaaccagg tgccggtgac tcacgagttt     780
atggttccca agaaagtggc gggaactgag agggcggaga cttctagaaa acgcccactg     840
gatgacgtca ccaataccaa ctataaaagt ccggagaagc gggcccggct ctcagttgtt     900
cctgagacgc ctcgcagttc agacgtgcct gtagagcccg ctcctctgcg acctctcaac     960
tggtcttcca ggtatgaatg cagatgtgac tatcatgcta aatttgactc tgtaacgggg    1020
gaatgtgacg agtgtgaata tttgaatcgg ggcaaaaatg ctgtatctt tcataatgct    1080
acacattgtc aaatttgtca cgctgttcct ccatgggaaa aggaaaatgt gtcagatttt    1140
aatgatttg atgactgtaa taaagagcag taa                                 1173
```

<210> 5
<211> 390
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 5
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Met Ala Leu Val Ser Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys
1               5                   10                  15
Gln Trp Ile Gln Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
            20                  25                  30
Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Ser Lys
        35                  40                  45
Ile Met Ser Leu Thr Lys Ser Ala Ser Asp Tyr Leu Val Gly Gln Thr
    50                  55                  60
Val Pro Glu Asp Ile Ser Glu Asn Arg Ile Trp Gln Ile Phe Asp Leu
65                  70                  75                  80
Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Val Leu Tyr Gly Trp Cys
                85                  90                  95
Thr Arg Ala Phe Gly Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
            100                 105                 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ser His Thr Val Pro
        115                 120                 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140
Cys Val Glu Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Ser
145                 150                 155                 160
Lys Val Val Glu Pro Ala Lys Ala Ile Leu Gly Gly Ser Arg Val Arg
                165                 170                 175
```

5

```
Val Asp Gln Lys Cys Lys Ser Ser Val Gln Val Asp Ser Thr Pro Val
              180                 185                 190
Ile Ile Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
              195                 200                 205
Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Arg Phe
              210                 215                 220
Glu Leu Met Arg Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln
225                           230                 235                 240
Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
              245                 250                 255
Thr His Glu Phe Met Val Pro Lys Lys Val Ala Gly Thr Glu Arg Ala
              260                 265                 270
Glu Thr Ser Arg Lys Arg Pro Leu Asp Asp Val Thr Asn Thr Asn Tyr
              275                 280                 285
Lys Ser Pro Glu Lys Arg Ala Arg Leu Ser Val Val Pro Glu Thr Pro
              290                 295                 300
Arg Ser Ser Asp Val Pro Val Glu Pro Ala Pro Leu Arg Pro Leu Asn
305                           310                 315                 320
Trp Ser Ser Arg Tyr Glu Cys Arg Cys Asp Tyr His Ala Lys Phe Asp
              325                 330                 335
Ser Val Thr Gly Glu Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys
              340                 345                 350
Asn Gly Cys Ile Phe His Asn Ala Thr His Cys Gln Ile Cys His Ala
              355                 360                 365
Val Pro Pro Trp Glu Lys Glu Asn Val Ser Asp Phe Asn Asp Phe Asp
370                           375                 380
Asp Cys Asn Lys Glu Gln
385                 390
```

```
<210> 6
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 6
atgtcttttg ttgaccaccc tccagattgg ttggaatcga tcggcgacgg ctttcgtgaa      60
tttctcggcc ttgaggcggg tcccccgaaa cccaaggcca atcaacagaa gcaagataac     120
gctcgaggtc ttgtgcttcc tgggtacaag tatcttggtc ctgggaacgg ccttgataag     180
ggcgatcctg tcaattttgc tgacgaggtt gcccgagagc acgacctctc ctaccagaaa     240
cagcttgagg cgggcgataa cccttacctc aagtacaacc acgcggacgc agagtttcag     300
gagaaactcg cttctgacac ttcttttggg ggaaaccttg ggaaggctgt tttccaggct     360
aaaaagagga ttctcgaacc tcttggcctg gttgagacgc cggataaaac ggcgcctgcg     420
gcaaaaaaga ggcctctaga gcagagtcct caagagccag actcctcgag cggagttggc     480
aagaaaggca aacagcctgc cagaaagaga ctcaactttg acgacgaacc tggagccgga     540
gacgggcctc ccccagaagg accatcttcc ggagctatgt ctactgagac tgaaatgcgt     600
gcagcagctg cggaaatggt ggcgatgcg ggacaaggtg ccgagggagt gggtaatgcc     660
tccggtgatt ggcattgcga ttccacttgg tcagagagcc acgtcaccac cacctcaacc     720
cgcacctggg tcctgccgac ctacaacaac cacctgtacc tgcggctcgg ctcgagcaac     780
gccagcgaca ccttcaacgg attctccacc ccctggggat actttgactt taaccgcttc     840
cactgccact ctcgccaag agactggcaa aggctcatca acaaccactg gggactgcgc     900
cccaaaagca tgcaagtccg catcttcaac atccaagtta aggaggtcac gacgtctaac     960
ggggagacga ccgtatccaa caacctcacc agcacggtcc agatctttgc ggacagcacg    1020
tacgagctcc cgtacgtgat ggatgcaggt caggagggca gcttgcctcc tttccccaac    1080
gacgtgttca tggtgcctca gtacgggtac tgcggactgg taaccggagg cagctctcaa    1140
aaccagacag acagaaatgc cttctactgt ctggagtact ttcccagcca gatgctgaga    1200
accggaaaca actttgagat ggtgtacaag tttgaaaacg tgcccttcca ctccatgtac    1260
gctcacagcc agagcctgga taggctgatg aacccgctgc tggaccagta cctgtgggag    1320
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ctccagtcta ccacctctgg aggaactctc aaccagggca attcagccac caactttgcc   1380
aagctgacca aaacaaactt ttctggctac cgcaaaaact ggctcccggg gcccatgatg   1440
aagcagcaga gattctccaa gactgccagt caaaactaca agattcccca gggaagaaac   1500
aacagtctgc tccattatga gaccagaact accctcgacg gaagatggag caattttgcc   1560
ccgggaacgg ccatggcaac cgcagccaac gacgccaccg acttctctca ggcccagctc   1620
atctttgcgg ggcccaacat caccggcaac accaccacag atgccaataa cctgatgttc   1680
acttcagaag atgaacttag ggccaccaac ccccgggaca ctgacctgtt tggccacctg   1740
gcaaccaacc agcaaaacgc caccaccgtt cctaccgtag acgacgtgga cggagtcggc   1800
gtgtacccgg gaatggtgtg gcaggacaga gacatttact accaagggcc catttgggcc   1860
aaaattccac acacggatgg acactttcac ccgtctcctc tcattggcgg atttggactg   1920
aaaagcccgc tccacaaat attcatcaaa aacactcctg tacccgccaa tcccgcaacg   1980
accttctctc cggccagaat caacagcttc atcacccagt acagcaccgg acaggtggct   2040
gtcaaaatag aatgggaaat ccagaaggag cggtccaaga gatggaaccc agaggtccag   2100
ttcacgtcca actacggagc acaggactcg cttctctggg ctcccgacaa cgccggagcc   2160
tacaaagagc ccagggccat tggatcccga tacctcacca accacctcta g           2211
```

<210> 7
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

```
<400> 7
Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Ser Ile Gly Asp
1               5                   10                  15
Gly Phe Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
                20                  25                  30
Ala Asn Gln Gln Lys Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
            35                  40                  45
Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Asp Pro Val
    50                  55                  60
Asn Phe Ala Asp Glu Val Ala Arg Glu His Asp Leu Ser Tyr Gln Lys
65                  70                  75                  80
Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95
Ala Glu Phe Gln Glu Lys Leu Ala Ser Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110
Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro Leu
        115                 120                 125
Gly Leu Val Glu Thr Pro Asp Lys Thr Ala Pro Ala Ala Lys Lys Arg
    130                 135                 140
Pro Leu Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160
Lys Lys Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Asp Asp Glu
                165                 170                 175
Pro Gly Ala Gly Asp Gly Pro Pro Glu Gly Pro Ser Ser Gly Ala
            180                 185                 190
Met Ser Thr Glu Thr Glu Met Arg Ala Ala Ala Gly Gly Asn Gly Gly
        195                 200                 205
Asp Ala Gly Gln Gly Ala Glu Gly Val Gly Asn Ala Ser Gly Asp Trp
    210                 215                 220
His Cys Asp Ser Thr Trp Ser Glu Ser His Val Thr Thr Thr Ser Thr
225                 230                 235                 240
Arg Thr Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu
                245                 250                 255
Gly Ser Ser Asn Ala Ser Asp Thr Phe Asn Gly Phe Ser Thr Pro Trp
            260                 265                 270
```

7

```
Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
        275             280             285
Trp Gln Arg Leu Ile Asn Asn His Trp Gly Leu Arg Pro Lys Ser Met
    290             295             300
Gln Val Arg Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn
305             310             315             320
Gly Glu Thr Thr Val Ser Asn Asn Leu Thr Ser Thr Val Gln Ile Phe
            325             330             335
Ala Asp Ser Thr Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu
        340             345             350
Gly Ser Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr
        355             360             365
Gly Tyr Cys Gly Leu Val Thr Gly Gly Ser Ser Gln Asn Gln Thr Asp
    370             375             380
Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
385             390             395             400
Thr Gly Asn Asn Phe Glu Met Val Tyr Lys Phe Glu Asn Val Pro Phe
            405             410             415
His Ser Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
        420             425             430
Leu Leu Asp Gln Tyr Leu Trp Glu Leu Gln Ser Thr Thr Ser Gly Gly
        435             440             445
Thr Leu Asn Gln Gly Asn Ser Ala Thr Asn Phe Ala Lys Leu Thr Lys
450             455             460
Thr Asn Phe Ser Gly Tyr Arg Lys Asn Trp Leu Pro Gly Pro Met Met
465             470             475             480
Lys Gln Gln Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro
            485             490             495
Gln Gly Arg Asn Asn Ser Leu Leu His Tyr Glu Thr Arg Thr Thr Leu
        500             505             510
Asp Gly Arg Trp Ser Asn Phe Ala Pro Gly Thr Ala Met Ala Thr Ala
        515             520             525
Ala Asn Asp Ala Thr Asp Phe Ser Gln Ala Gln Leu Ile Phe Ala Gly
    530             535             540
Pro Asn Ile Thr Gly Asn Thr Thr Thr Asp Ala Asn Asn Leu Met Phe
545             550             555             560
Thr Ser Glu Asp Glu Leu Arg Ala Thr Asn Pro Arg Asp Thr Asp Leu
            565             570             575
Phe Gly His Leu Ala Thr Asn Gln Gln Asn Ala Thr Thr Val Pro Thr
        580             585             590
Val Asp Asp Val Asp Gly Val Gly Val Tyr Pro Gly Met Val Trp Gln
    595             600             605
Asp Arg Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610             615             620
Thr Asp Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu
625             630             635             640
Lys Ser Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala
            645             650             655
Asn Pro Ala Thr Thr Phe Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr
            660             665             670
Gln Tyr Ser Thr Gly Gln Val Ala Val Lys Ile Glu Trp Glu Ile Gln
        675             680             685
Lys Glu Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn
    690             695             700
Tyr Gly Ala Gln Asp Ser Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala
705             710             715             720
Tyr Lys Glu Pro Arg Ala Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
            725             730             735
```

<210> 8
<211> 1803

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 8
```
acggcgcctg cggcaaaaaa gaggcctcta gagcagagtc ctcaagagcc agactcctcg    60
agcggagttg gcaagaaagg caaacagcct gccagaaaga gactcaactt tgacgacgaa   120
cctggagccg gagacgggcc tcccccagaa ggaccatctt ccggagctat gtctactgag   180
actgaaatgc gtgcagcagc tggcggaaat ggtggcgatg cgggacaagg tgccgaggga   240
gtgggtaatg cctccggtga ttggcattgc gattccactt ggtcagagag ccacgtcacc   300
accacctcaa cccgcacctg ggtcctgccg acctacaaca accacctgta cctgcggctc   360
ggctcgagca cgccagcga caccttcaac ggattctcca ccccctgggg atactttgac   420
tttaaccgct tccactgcca cttctcgcca agagactggc aaaggctcat caacaaccac   480
tggggactgc gccccaaaag catgcaagtc cgcatcttca acatccaagt taaggaggtc   540
acgacgtcta acggggagac gaccgtatcc aacaacctca ccagcacggt ccagatcttt   600
gcggacagca cgtacgagct cccgtacgtg atggatgcag gtcaggaggg cagcttgcct   660
cctttcccca acgacgtgtt catggtgcct cagtacgggt actgcggact ggtaaccgga   720
ggcagctctc aaaaccagac agacagaaat gccttctact gtctggagta ctttcccagc   780
cagatgctga gaaccggaaa caactttgag atggtgtaca agtttgaaaa cgtgcccttc   840
cactccatgt acgctcacag ccagagcctg ataggctga tgaacccgct gctggaccag   900
tacctgtggg agctccagtc taccacctct ggaggaactc tcaaccaggg caattcagcc   960
accaactttg ccaagctgac caaaacaaac ttttctggct accgcaaaaa ctggctcccg   1020
gggcccatga tgaagcagca gagattctcc aagactgcca gtcaaaacta caagattccc   1080
cagggaagaa acaacagtct gctccattat gagaccagaa ctaccctcga cggaagatgg   1140
agcaattttg ccccgggaac ggccatggca accgcagcca acgacgccac cgacttctct   1200
caggcccagc tcatctttgc ggggcccaac atcaccggca acaccaccac agatgccaat   1260
aacctgatgt tcacttcaga agatgaactt agggccacca accccgggga cactgacctg   1320
tttggccacc tggcaaccaa ccagcaaaac gccaccaccg ttcctaccgt agacgacgtg   1380
gacggagtcg gcgtgtaccc gggaatggtg tggcaggaca gagacattta ctaccaaggg   1440
cccatttggg ccaaaattcc acacacggat ggacactttc acccgtctcc tctcattggc   1500
ggatttggac tgaaaagccc gcctccacaa atattcatca aaaacactcc tgtacccgcc   1560
aatcccgcaa cgaccttctc tccggccaga atcaacagct tcatcaccca gtacagcacc   1620
ggacaggtgg ctgtcaaaat agaatgggaa atccagaagg agcggtccaa gagatggaac   1680
ccagaggtcc agttcacgtc caactacgga gcacaggact cgcttctctg ggctcccgac   1740
aacgccggag cctacaaaga gcccagggcc attggatccc gatacctcac caaccacctc   1800
tag                                                                  1803
```

<210> 9
<211> 600
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 9
```
Thr Ala Pro Ala Ala Lys Lys Arg Pro Leu Glu Gln Ser Pro Gln Glu
1               5                   10                  15
Pro Asp Ser Ser Ser Gly Val Gly Lys Lys Gly Lys Gln Pro Ala Arg
            20                  25                  30
Lys Arg Leu Asn Phe Asp Asp Glu Pro Gly Ala Gly Asp Gly Pro Pro
        35                  40                  45
Pro Glu Gly Pro Ser Ser Gly Ala Met Ser Thr Glu Thr Glu Met Arg
    50                  55                  60
Ala Ala Ala Gly Gly Asn Gly Gly Asp Ala Gly Gln Gly Ala Glu Gly
65                  70                  75                  80
```

```
Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp Ser Glu
                85                  90                  95
Ser His Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro Thr Tyr
                100                 105                 110
Asn Asn His Leu Tyr Leu Arg Leu Gly Ser Ser Asn Ala Ser Asp Thr
                115                 120                 125
Phe Asn Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        130                 135                 140
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn His
145                 150                 155                 160
Trp Gly Leu Arg Pro Lys Ser Met Gln Val Arg Ile Phe Asn Ile Gln
                165                 170                 175
Val Lys Glu Val Thr Thr Ser Asn Gly Glu Thr Thr Val Ser Asn Asn
                180                 185                 190
Leu Thr Ser Thr Val Gln Ile Phe Ala Asp Ser Thr Tyr Glu Leu Pro
                195                 200                 205
Tyr Val Met Asp Ala Gly Gln Glu Gly Ser Leu Pro Pro Phe Pro Asn
        210                 215                 220
Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Leu Val Thr Gly
225                 230                 235                 240
Gly Ser Ser Gln Asn Gln Thr Asp Arg Asn Ala Phe Tyr Cys Leu Glu
                245                 250                 255
Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Met Val
                260                 265                 270
Tyr Lys Phe Glu Asn Val Pro Phe His Ser Met Tyr Ala His Ser Gln
                275                 280                 285
Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp Gln Tyr Leu Trp Glu
        290                 295                 300
Leu Gln Ser Thr Thr Ser Gly Gly Thr Leu Asn Gln Gly Asn Ser Ala
305                 310                 315                 320
Thr Asn Phe Ala Lys Leu Thr Lys Thr Asn Phe Ser Gly Tyr Arg Lys
                325                 330                 335
Asn Trp Leu Pro Gly Pro Met Met Lys Gln Gln Arg Phe Ser Lys Thr
                340                 345                 350
Ala Ser Gln Asn Tyr Lys Ile Pro Gln Gly Arg Asn Asn Ser Leu Leu
                355                 360                 365
His Tyr Glu Thr Arg Thr Thr Leu Asp Gly Arg Trp Ser Asn Phe Ala
        370                 375                 380
Pro Gly Thr Ala Met Ala Thr Ala Ala Asn Asp Ala Thr Asp Phe Ser
385                 390                 395                 400
Gln Ala Gln Leu Ile Phe Ala Gly Pro Asn Ile Thr Gly Asn Thr Thr
                405                 410                 415
Thr Asp Ala Asn Asn Leu Met Phe Thr Ser Glu Asp Glu Leu Arg Ala
                420                 425                 430
Thr Asn Pro Arg Asp Thr Asp Leu Phe Gly His Leu Ala Thr Asn Gln
        435                 440                 445
Gln Asn Ala Thr Thr Val Pro Thr Val Asp Asp Val Asp Gly Val Gly
        450                 455                 460
Val Tyr Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Tyr Gln Gly
465                 470                 475                 480
Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser
                485                 490                 495
Pro Leu Ile Gly Gly Phe Gly Leu Lys Ser Pro Pro Pro Gln Ile Phe
                500                 505                 510
Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala Thr Thr Phe Ser Pro
                515                 520                 525
Ala Arg Ile Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ala
        530                 535                 540
Val Lys Ile Glu Trp Glu Ile Gln Lys Glu Arg Ser Lys Arg Trp Asn
545                 550                 555                 560
```

10

Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Ala Gln Asp Ser Leu Leu
              565   570   575
Trp Ala Pro Asp Asn Ala Gly Ala Tyr Lys Glu Pro Arg Ala Ile Gly
              580   585   590
Ser Arg Tyr Leu Thr Asn His Leu
              595   600

<210> 10
<211> 1617
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 10
atgcgtgcag cagctggcgg aaatggtggc gatgcgggac aaggtgccga gggagtgggt   60
aatgcctccg gtgattggca ttgcgattcc acttggtcag agagccacgt caccaccacc   120
tcaacccgca cctgggtcct gccgacctac aacaaccacc tgtacctgcg gctcggctcg   180
agcaacgcca gcgacacctt caacggattc tccacccccct ggggatactt tgactttaac   240
cgcttccact gccacttctc gccaagagac tggcaaaggc tcatcaacaa ccactgggga   300
ctgcgcccca aaagcatgca agtccgcatc ttcaacatcc aagttaagga ggtcacgacg   360
tctaacgggg agacgaccgt atccaacaac ctcaccagca cggtccagat ctttgcggac   420
agcacgtacg agctcccgta cgtgatggat gcaggtcagg agggcagctt gcctcctttc   480
cccaacgacg tgttcatggt gcctcagtac gggtactgcg gactggtaac cggaggcagc   540
tctcaaaacc agacagacag aaatgccttc tactgtctgg agtactttcc cagccagatg   600
ctgagaaccg gaaacaactt tgagatggtg tacaagtttg aaaacgtgcc cttccactcc   660
atgtacgctc acagccagag cctggatagg ctgatgaacc cgctgctgga ccagtacctg   720
tgggagctcc agtctaccac ctctggagga actctcaacc agggcaattc agccaccaac   780
tttgccaagc tgaccaaaac aaacttttct ggctaccgca aaaactggct cccgggggccc   840
atgatgaagc agcagagatt ctccaagact gccagtcaaa actacaagat tccccaggga   900
agaaacaaca gtctgctcca ttatgagacc agaactaccc tcgacggaag atggagcaat   960
tttgccccgg aacggccat ggcaaccgca gccaacgacg ccaccgactt ctctcaggcc   1020
cagctcatct ttgcggggcc caacatcacc ggcaacacca ccacagatgc caataacctg   1080
atgttcactt cagaagatga acttagggcc accaaccccc gggacactga cctgtttggc   1140
cacctggcaa ccaaccagca aaacgccacc accgttccta ccgtagacga cgtggacgga   1200
gtcggcgtgt acccgggaat ggtgtggcag gacagagaca tttactacca agggcccatt   1260
tgggccaaaa ttccacacac ggatggacac tttcacccgt ctcctctcat tggcggattt   1320
ggactgaaaa gcccgcctcc acaaatattc atcaaaaaca ctcctgtacc cgccaatccc   1380
gcaacgacct ctctccggc cagaatcaac agcttcatca cccagtacag caccggacag   1440
gtggctgtca aaatagaatg ggaaatccag aaggagcggt ccaagagatg gaacccagag   1500
gtccagttca cgtccaacta cggagcacag gactcgcttc tctgggctcc cgacaacgcc   1560
ggagcctaca agagcccag ggccattgga tcccgatacc tcaccaacca cctctag   1617

<210> 11
<211> 538
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 11
Met Arg Ala Ala Ala Gly Gly Asn Gly Gly Asp Ala Gly Gln Gly Ala
1   5   10   15
Glu Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
              20   25   30
Ser Glu Ser His Val Thr Thr Thr Ser Thr Arg Thr Trp Val Leu Pro
          35   40   45

```
Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Ser Ser Asn Ala Ser
    50              55              60
Asp Thr Phe Asn Gly Phe Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
65              70              75              80
Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
            85              90              95
Asn His Trp Gly Leu Arg Pro Lys Ser Met Gln Val Arg Ile Phe Asn
        100             105             110
Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu Thr Thr Val Ser
        115             120             125
Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp Ser Thr Tyr Glu
    130             135             140
Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser Leu Pro Pro Phe
145             150             155             160
Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Leu Val
            165             170             175
Thr Gly Gly Ser Ser Gln Asn Gln Thr Asp Arg Asn Ala Phe Tyr Cys
        180             185             190
Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu
        195             200             205
Met Val Tyr Lys Phe Glu Asn Val Pro Phe His Ser Met Tyr Ala His
    210             215             220
Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp Gln Tyr Leu
225             230             235             240
Trp Glu Leu Gln Ser Thr Thr Ser Gly Gly Thr Leu Asn Gln Gly Asn
            245             250             255
Ser Ala Thr Asn Phe Ala Lys Leu Thr Lys Thr Asn Phe Ser Gly Tyr
        260             265             270
Arg Lys Asn Trp Leu Pro Gly Pro Met Met Lys Gln Gln Arg Phe Ser
        275             280             285
Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Gln Gly Arg Asn Asn Ser
    290             295             300
Leu Leu His Tyr Glu Thr Arg Thr Thr Leu Asp Gly Arg Trp Ser Asn
305             310             315             320
Phe Ala Pro Gly Thr Ala Met Ala Thr Ala Ala Asn Asp Ala Thr Asp
            325             330             335
Phe Ser Gln Ala Gln Leu Ile Phe Ala Gly Pro Asn Ile Thr Gly Asn
        340             345             350
Thr Thr Thr Asp Ala Asn Asn Leu Met Phe Thr Ser Glu Asp Glu Leu
    355             360             365
Arg Ala Thr Asn Pro Arg Asp Thr Asp Leu Phe Gly His Leu Ala Thr
    370             375             380
Asn Gln Gln Asn Ala Thr Thr Val Pro Thr Val Asp Asp Val Asp Gly
385             390             395             400
Val Gly Val Tyr Pro Gly Met Val Trp Gln Asp Arg Asp Ile Tyr Tyr
            405             410             415
Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His
            420             425             430
Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys Ser Pro Pro Pro Gln
        435             440             445
Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala Thr Thr Phe
    450             455             460
Ser Pro Ala Arg Ile Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln
465             470             475             480
Val Ala Val Lys Ile Glu Trp Glu Ile Gln Lys Glu Arg Ser Lys Arg
            485             490             495
Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Ala Gln Asp Ser
        500             505             510
Leu Leu Trp Ala Pro Asp Asn Ala Gly Ala Tyr Lys Glu Pro Arg Ala
        515             520             525
```

Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
    530   535

<210> 12
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 12
gtggcactcc cccccctgtc gcgttcgctc gttcgctggc tcgattgggg gggtggcagc   60
tcaaagagct gccagacgac ggccctctgg gccgtcgccc ccccaatcga gccagcgaac   120
gagcgaacgc gacagggggg ggagtgccac   150

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 13
ctctagcaag ggggttttgt   20

<210> 14
<211> 7
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 14
agtgtgg   7

<210> 15
<211> 158
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 15
aggtggtgat gtcattgttg atgtcattat agttgtcacg cgatagttaa tgattaacag   60
tcatgtgatg tgtgttatcc aataggatga aagcgcgcga atgagatctc gcgagacttc   120
cggggtataa aaggggtgag tgaacgagcc cgccgcca   158

<210> 16
<211> 112
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 16
ggtggattct gggtatattc ccgcctacct gctgccgaag gtccaaccag agcttcagtg   60
ggcgtggact aacctcgaag agtataaatt ggccgccctc aatctggagg ag   112

<210> 17
<211> 169
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 17
agtcaaagac tttttttgctt gggcaaaggt caaccaggtg ccggtgactc acgagtttat   60
ggttcccaag aaagtggcgg gaactgagag ggcggagact tctagaaaac gcccactgga   120
tgacgtcacc aataccaact ataaaagtcc ggagaagcgg gcccggctc   169

<210> 18
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct ·

<400> 18
Gly Ser Ser Asn Ala Ser Asp Thr
 1   5

<210> 19
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 19
Thr Thr Ser Gly Gly Thr Leu Asn Gln Gly Asn Ser Ala Thr
 1   5   10

<210> 20
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 20
Asn Gly Arg Ala His Ala
 1   5

<210> 21

```
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 21
Ser Ile Gly Tyr Pro Leu Pro
 1                   5

<210> 22
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 22
Lys Phe Asn Lys Pro Phe Val Phe Leu Ile
 1               5                   10

<210> 23
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note=synthetic
      construct

<400> 23
Asn Ile Ser Leu Asp Asn Pro Leu Glu Asn Pro Ser Ser Leu Phe Asp
 1               5                   10                  15
Leu Val Ala Arg Ile Lys
            20
```